

We claim:

1. A method for altering fiber development or properties of a fiber-producing plant comprising providing cells of said plants with a chimeric gene comprising the following operably linked DNA fragments:

- 5 a plant expressible promoter;
- a coding region which when transcribed yields an RNA said RNA being capable of reducing the expression of an endogenous sucrose synthase gene, preferably an endogenous sucrose synthase gene expressed in fiber cells, preferably fiber initial cells; or
- 10 capable of being translated into an active sucrose synthase protein; and
- a transcription termination and polyadenylation signal which functions in said plant cells.

15 2. The method according to claim 1, wherein said RNA is capable of being translated into an active sucrose synthase protein.

3. The method according to claim 2, wherein said coding region comprises a nucleotide sequence selected from

- 20 a) a nucleotide sequence encoding a polypeptide comprising the amino acid sequence of SEQ ID No 2;
- b) a nucleotide sequence comprising the nucleotide sequence of SEQ ID No 1;
- c) a nucleotide sequence having at least 70% sequence identity with
- 25 the nucleotide sequence a) or b);
- d) a nucleotide sequence hybridizing under stringent conditions with the nucleotide sequence a) or b);
- or a part thereof encoding an active sucrose synthase.

30 4. The method according to claim 1, wherein said RNA is capable of reducing the expression of an endogenous sucrose synthase gene.

30456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

5. The method according to claim 4, wherein said coding region comprises a nucleotide sequence selected from the group consisting of
- 5 a nucleotide sequence comprising at least 19 or 25 contiguous nucleotides having at least 70 % sequence identity to a nucleotide sequence encoding a polypeptide comprising the amino acid sequence of SEQ ID No 2 or the complement thereof; and
- 10 a nucleotide sequence comprising at least 25 contiguous nucleotides having at least 70 % sequence identity to a nucleotide sequence encoding a polypeptide comprising the nucleotide sequence of SEQ ID No 1 or the complement thereof.
6. The method according to claim 5, wherein said coding region comprises the nucleotide sequence of SEQ ID No 1 from the nucleotide at position 2208
- 15 to the nucleotide at position 2598 or the complement thereof.
7. The method according to claim 5, wherein said coding region comprises both sense and antisense nucleotide sequences capable of forming a double stranded RNA molecule.
- 20 8. The method according to any one of claims 1 to 7, wherein said promoter is a subterranean clover stunt virus promoter.
9. The method according to any one of claims 1 to 7, wherein said fiber-
- 25 producing plant is a cotton plant.
10. The method according to claim 8, wherein said fiber-producing plant is a cotton plant.
- 30 11. The method according to claim 9, wherein said cotton plant is a Fibermax<sup>TM</sup> variety.

12. A method for improving fiber yield in a fiber-producing plant, comprising providing cells of said plant with a chimeric gene comprising the following operably linked DNA fragments

- 5           a plant expressible promoter;  
            a DNA region capable of being translated into an active sucrose  
            synthase protein; and  
            a transcription termination and polyadenylation signal which functions in  
            said plant cells.

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13. A method for improving fiber quality in a fiber-producing plant, comprising providing cells of said plant with a chimeric gene comprising the following operably linked DNA fragments

- a plant expressible promoter;  
15           a DNA region capable of being translated into an active sucrose  
            synthase protein; and  
            a transcription termination and polyadenylation signal which functions in  
            said plant cells.

20   14. A method for increasing seed size in a fiber-producing plant, comprising providing cells of said plant with a chimeric gene comprising the following operably linked DNA fragments:

- a seed-specific promoter;  
            a DNA region capable of being translated into an active sucrose  
25           synthase protein; and  
            a transcription termination and polyadenylation signal which functions in  
            said plant cells.

15. A fiber-producing plant comprising in its genome a chimeric DNA  
30 comprising the following operably linked DNA fragments:  
            a plant expressible promoter;

a coding region which when transcribed yields an RNA said RNA being capable of reducing the expression of an endogenous sucrose synthase gene, preferably an endogenous sucrose synthase gene expressed in fiber cells, preferably fiber initial cells; or

5        capable of being translated into an active sucrose synthase protein; and

a transcription termination and polyadenylation signal which functions in said plant cells.

10    16. A fiber-producing plant according to claim 15, wherein said RNA is capable of increasing the expression of an endogenous sucrose synthase gene, preferably an endogenous sucrose synthase gene expressed in fiber cells, preferably fiber initial cells and said fiber cells have an increased sucrose synthase activity compared to fiber cells of plant cells which do not comprise

15    said chimeric DNA.

17. The fiber-producing plant according to claim 16, wherein said coding region comprises a nucleotide sequence selected from

20        a) a nucleotide sequence encoding a polypeptide comprising the amino acid sequence of SEQ ID No 2;

      b) a nucleotide sequence comprising the nucleotide sequence of SEQ ID No 1;

      c) a nucleotide sequence having at least 70% sequence identity with the nucleotide sequence a) or b);

25        d) a nucleotide sequence hybridizing under stringent conditions with the nucleotide sequence a) or b);

or a part thereof encoding an active sucrose synthase.

18. A fiber-producing plant according to claim 15, wherein said RNA is

30    capable of reducing an endogenous sucrose synthase gene and said fiber cells

have a reduced sucrose synthase activity compared to fiber cells of plant cells which do not comprise said chimeric DNA.

19. The fiber-producing plant according to claim 18, wherein said coding  
 5 region comprises a nucleotide sequence selected from the group consisting of  
 a nucleotide sequence comprising at least 19 or 25 contiguous  
 nucleotides having at least 70 % sequence identity to a nucleotide  
 sequence encoding a polypeptide comprising the amino acid sequence  
 of SEQ ID No 2 or the complement thereof; and  
 10 a nucleotide sequence comprising at least 19 or 25 contiguous  
 nucleotides having at least 70 % sequence identity to a nucleotide  
 sequence encoding a polypeptide comprising the nucleotide sequence of  
 SEQ ID No 1 or the complement thereof.
- 15 20. The fiber-producing plant according to claim 18, wherein said coding  
 region comprises the nucleotide sequence of SEQ ID No 1 from the nucleotide  
 at position 2208 to the nucleotide at position 2598 or the complement thereof.
21. The fiber-producing plant according to any one of claims 15 to 20,  
 20 wherein said plant is a cotton plant.
22. Seeds of a plant according to any one of claims 15 to 20.
23. Seeds of a plant according to claim 21.
- 25 24. Fibers with altered development or properties, isolated from plants  
 according to any one of claims 15 to 20.
25. Fibers with altered development or properties, isolated from plants  
 30 according to claim 21.

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